

IN THE SEQUENCE LISTING:

Please amend the sequence listing to add SEQ ID NOS; 35-38 as follows:

<210> 35
<211> 1749
<212> DNA
<213> Arabidopsis thaliana

<400> 35
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GTTGAGGATA AAAATTTCCA AGCTGCAGAG AGATGGGCTA CCTTCATGGG AAGCCAAGT 720
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GTTGATGAAC TGTGCGATCG ATATTCACCT CAAGGGCTGC CAAAAGCACG AGAGGCTGAG 1020
GTTGCTTTTG TTGAAAAAAG CTTTCTGCGT CTCAACGATC TAGCTGTAGA AGATGTAGTT 1080
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<211> 582
<212> PRT
<213> Arabidopsis thaliana

<400> 36
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35 40 45
His Gly Ser Leu Lys Ala Thr Lys Lys Phe Gln Ala Leu Gln Tyr Gln
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Val	His	Arg	Val	Leu	Ala	Asn	Lys	Pro	Gln	Pro	Gly	Pro	Ala	Thr	Phe	65	70	75	80
Ile	Ile	Asn	Cys	Leu	Thr	Leu	Leu	Pro	Leu	Phe	Gly	Val	Tyr	Gly	Glu	85	90	95	
Gly	Phe	Ser	His	Leu	Val	Ile	Ser	Ala	Leu	Arg	Arg	Phe	Phe	Lys	Thr	100	105	110	
Val	Ser	Glu	Pro	Thr	Ser	Glu	Glu	Asp	Ile	Cys	Leu	Ala	Arg	Lys	Leu	115	120	125	
Ala	Ala	Gln	Phe	Phe	Leu	Ala	Thr	Val	Gly	Gly	Ser	Leu	Thr	Tyr	Asp	130	135	140	
Glu	Lys	Val	Met	Val	His	Thr	Leu	Arg	Val	Phe	Asp	Val	Arg	Leu	Thr	145	150	155	160
Ser	Ile	Asp	Glu	Ala	Leu	Ser	Ile	Ser	Glu	Val	Trp	Gln	Arg	Tyr	Gly	165	170	175	
Phe	Ala	Cys	Gly	Asn	Ala	Phe	Leu	Glu	Gln	Tyr	Ile	Ser	Asp	Leu	Ile	180	185	190	
Lys	Ser	Lys	Ser	Phe	Met	Thr	Ala	Val	Thr	Leu	Leu	Glu	His	Phe	Ser	195	200	205	
Phe	Arg	Phe	Pro	Gly	Glu	Thr	Phe	Leu	Gln	Gln	Met	Val	Glu	Asp	Lys	210	215	220	
Asn	Phe	Gln	Ala	Ala	Glu	Arg	Trp	Ala	Thr	Phe	Met	Gly	Arg	Pro	Ser	225	230	235	240
Leu	Cys	Ile	Leu	Val	Gln	Glu	Tyr	Gly	Ser	Arg	Asn	Met	Leu	Lys	Gln	245	250	255	
Ala	Tyr	Asn	Ile	Ile	Asn	Lys	Asn	Tyr	Leu	Gln	His	Asp	Phe	Pro	Glu	260	265	270	
Leu	Tyr	His	Lys	Cys	Lys	Glu	Ser	Ala	Leu	Lys	Val	Leu	Ala	Glu	Lys	275	280	285	
Ala	Cys	Trp	Asp	Val	Ala	Glu	Ile	Lys	Thr	Lys	Gly	Asp	Arg	Gln	Leu	290	295	300	
Leu	Lys	Tyr	Leu	Val	Tyr	Leu	Ala	Val	Glu	Ala	Gly	Tyr	Leu	Glu	Lys	305	310	315	320
Val	Asp	Glu	Leu	Cys	Asp	Arg	Tyr	Ser	Leu	Gln	Gly	Leu	Pro	Lys	Ala	325	330	335	
Arg	Glu	Ala	Glu	Val	Ala	Phe	Val	Glu	Lys	Ser	Phe	Leu	Arg	Leu	Asn	340	345	350	
Asp	Leu	Ala	Val	Glu	Asp	Val	Val	Trp	Val	Asp	Glu	Val	Asn	Glu	Leu	355	360	365	

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 Ser Ile Met Gln Ile Gly Ser Asp Thr Lys Ile Phe Ile Leu Asp Leu
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 Tyr Asp Met Leu Leu Asp Ile Gln Asn Val Phe Asn Glu Pro Phe Gly
 485 490 495
 Gly Leu Ala Gly Leu Thr Lys Lys Ile Leu Gly Val Ser Leu Asn Lys
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<210> 37
 <211> 1518
 <212> DNA
 <213> Arabidopsis thaliana

<400> 37
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 CACGCCACGG ATGTCTCCGA TGTCTTCCTC ATTGATTGTA GTTCGATTCA TCTTCCATCG 240
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AAGGCTACAG	ATGTAATCAG	ATCAATGTCG	GAAAATGGTC	AAAACATAGC	CAATGGAGTG	780
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AGGAAGTTTG	GAGAACGGAT	CCTGTTGAAG	GAGTCTGATC	TTCTACCAAA	GAAACTTAAG	900
AAGAAAACAA	GAAGACGTGT	CGCCTCAAGC	ACTATGAACA	CAAATAAGCA	GTTGGTCTGT	960
TCTGCGGACT	GGCAAGGTCC	ACCGCCATGG	GACTCATCTT	TAGGCGGTGA	TGGCTGCCCT	1020
AAATTTCTAT	TGGATGTGAT	GGTTGAAGGT	TTGGCGAAAC	ATCTACGTTG	TGTGGGGATT	1080
GATGCTGCAA	TCCACACTC	AAAGAAGCCG	GATTCAAGGG	AGTTGCTTGA	TCAAGCATTG	1140
AAAGAGAACA	GAGTTCTATT	AACAAGAGAT	ACAAAATTGT	TGAGACACCA	GGATTTGGCA	1200
AAGCATCAAA	TATATCGAGT	AAAGAGTCTT	CTTAAAAATG	AGCAGCTACT	TGAGGTGATA	1260
GAGACTTTCC	AGCTAAAGAT	CAGCGGAAAT	CAGCTGATGT	CCAGATGTAC	GAAGTGCAAT	1320
GGGAAATTTA	TTCAGAAACC	TCTAAGCATT	GAAGAAGCTA	TTGAAGCAGC	AAAGGGTTTC	1380
CAAAGAATAC	CCAACTGCTT	ATTTAACAAA	AATTTAGAGT	TTTGGCAGTG	CATGAACTGC	1440
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<210> 38

<211> 505

<212> PRT

<213> Arabidopsis thaliana

<400> 38

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			20					25					30		

Leu	Asp	Ala	Glu	Trp	Lys	Pro	Gln	His	Ser	Asn	Thr	Ser	Ser	Phe	Pro
		35					40					45			

Thr	Val	Thr	Leu	Leu	Gln	Val	Ala	Cys	Arg	Leu	Ser	His	Ala	Thr	Asp
	50					55					60				

Val	Ser	Asp	Val	Phe	Leu	Ile	Asp	Leu	Ser	Ser	Ile	His	Leu	Pro	Ser
65					70					75				80	

Val	Trp	Glu	Leu	Leu	Asn	Asp	Met	Phe	Val	Ser	Pro	Asp	Val	Leu	Lys
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Leu	Gly	Phe	Arg	Phe	Lys	Gln	Asp	Leu	Val	Tyr	Leu	Ser	Ser	Thr	Phe
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Thr	Gln	His	Gly	Cys	Glu	Gly	Gly	Phe	Gln	Glu	Val	Lys	Gln	Tyr	Leu
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Asp	Ile	Thr	Ser	Ile	Tyr	Asn	Tyr	Leu	Gln	His	Lys	Arg	Phe	Gly	Arg
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Lys	Ala	Pro	Lys	Asp	Ile	Lys	Ser	Leu	Ala	Ala	Ile	Cys	Lys	Glu	Met
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Leu	Asp	Ile	Ser	Leu	Ser	Lys	Glu	Leu	Gln	Cys	Ser	Asp	Trp	Ser	Tyr
				165					170					175	

Arg	Pro	Leu	Thr	Glu	Glu	Gln	Lys	Leu	Tyr	Ala	Ala	Thr	Asp	Ala	His
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			180					185					190			
Cys	Leu	Leu	Gln	Ile	Phe	Asp	Val	Phe	Glu	Ala	His	Leu	Val	Glu	Gly	
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Ile	Thr	Val	Gln	Asp	Leu	Arg	Val	Ile	Asn	Val	Gly	Leu	Gln	Glu	Ile	
	210					215					220					
Leu	Thr	Glu	Ser	Asp	Tyr	Ser	Ser	Lys	Ile	Val	Thr	Val	Lys	Leu	Cys	
225					230					235					240	
Lys	Ala	Thr	Asp	Val	Ile	Arg	Ser	Met	Ser	Glu	Asn	Gly	Gln	Asn	Ile	
				245					250					255		
Ala	Asn	Gly	Val	Val	Pro	Arg	Lys	Thr	Thr	Leu	Asn	Thr	Met	Pro	Met	
			260					265					270			
Asp	Glu	Asn	Leu	Leu	Lys	Ile	Val	Arg	Lys	Phe	Gly	Glu	Arg	Ile	Leu	
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Leu	Lys	Glu	Ser	Asp	Leu	Leu	Pro	Lys	Lys	Leu	Lys	Lys	Lys	Thr	Arg	
	290					295					300					
Arg	Arg	Val	Ala	Ser	Ser	Thr	Met	Asn	Thr	Asn	Lys	Gln	Leu	Val	Cys	
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Ser	Ala	Asp	Trp	Gln	Gly	Pro	Pro	Pro	Trp	Asp	Ser	Ser	Leu	Gly	Gly	
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Asp	Gly	Cys	Pro	Lys	Phe	Leu	Leu	Asp	Val	Met	Val	Glu	Gly	Leu	Ala	
			340					345					350			
Lys	His	Leu	Arg	Cys	Val	Gly	Ile	Asp	Ala	Ala	Ile	Pro	His	Ser	Lys	
		355					360					365				
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	370					375					380					
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Lys	His	Gln	Ile	Tyr	Arg	Val	Lys	Ser	Leu	Leu	Lys	Asn	Glu	Gln	Leu	
				405					410					415		
Leu	Glu	Val	Ile	Glu	Thr	Phe	Gln	Leu	Lys	Ile	Ser	Gly	Asn	Gln	Leu	
			420					425					430			
Met	Ser	Arg	Cys	Thr	Lys	Cys	Asn	Gly	Lys	Phe	Ile	Gln	Lys	Pro	Leu	
		435					440					445				
Ser	Ile	Glu	Glu	Ala	Ile	Glu	Ala	Ala	Lys	Gly	Phe	Gln	Arg	Ile	Pro	
	450					455					460					
Asn	Cys	Leu	Phe	Asn	Lys	Asn	Leu	Glu	Phe	Trp	Gln	Cys	Met	Asn	Cys	
465					470					475					480	
His	Gln	Leu	Tyr	Trp	Glu	Gly	Thr	Gln	Tyr	His	Asn	Ala	Val	Gln	Lys	

				485				490				495
Phe	Met	Glu	Val	Cys	Lys	Leu	Ser	Glu				
			500					505				